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<110> Ono Pharmaceutical Co., Ltd.
<120> Novel Polypeptides, cDNA encoding the same, and use of them
<130> Q61459
<140> 09/700,397
<141> 2000-11-14
<150> JP 10-131815
<151> 1998-05-14
<150> PCT/JP99/02485
<151> 1999-05-13
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<170> PatentIn version 3.0
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Tyr Thr Cys Ser Val Gln Thr Asp Asn His Pro Lys Thr Ser Arg Val
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His Leu Ile Val Gln Val Ser Pro Lys Ile Val Glu Ile Ser Ser Asp
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Ile Ser Ile Asn Glu Gly Asn Asn Ile Ser Leu Thr Cys Ile Ala Thr
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Thr Gln Tyr Ser Ile Glu Ile Gln Asn Val Asp Val Tyr Asp Glu Gly
65 70 75 80

Pro Tyr Thr Cys Ser Val Gln Thr Asp Asn His Pro Lys Thr Ser Arg
85 90 95

Val His Leu Ile Val Gln Val Ser Pro Lys Ile Val Glu Ile Ser Ser
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Thr Asn Ala Ser Ile Met Leu Phe Gly Pro Gly Ala Val Ser Glu Val
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Arg Cys Leu Arg Lys Arg Ser Thr Val Ser Phe Leu Gly Val Leu Val
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Ile Phe Leu Leu Phe Met Asn Leu Tyr Ile Glu Asp Ser Tyr Val Leu
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Glu Gly Asp Lys Gln Leu Ile Arg Glu Thr Ser Thr His Gln Leu Asn
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Leu Glu Gly Asp Lys Gln Leu Ile Arg Glu Thr Ser Thr His Gln Leu
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Asn Ser Glu Arg Tyr Val His Thr Phe Lys Asp Leu Ser Asn Phe Ser
65 70 75 80

Gly Ala Ile Asn Val Thr Tyr Arg Tyr Leu Ala Ala Thr Pro Leu Gln
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Arg Lys Arg Tyr Leu Thr Ile Gly Leu Ser Ser Val Lys Arg Lys Lys
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Gly Asn Tyr Leu Leu Glu Thr Ile Lys Ser Ile Phe Glu Gln Ser Ser

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120

125

Tyr Glu Glu Leu Lys Glu Ile Ser Val Val Ile His Leu Ala Asp Phe
130 135 140

Asn Ser Ser Trp Arg Asp Ala Met Val Gln Asp Ile Thr Gln Lys Phe
145 150 155 160

Ala His His Ile Ile Ala Gly Arg Leu Met Val Ile His Ala Pro Glu
165 170 175

Glu Tyr Tyr Pro Ile Leu Asp Gly Leu Lys Arg Asn Tyr Asn Asp Pro
180 185 190

Glu Asp Arg Val Lys Phe Arg Ser Lys Gln Asn Val Asp Tyr Thr Phe
195 200 205

Leu Leu Asn Phe Cys Ala Asn Thr Ser Asp Tyr Tyr Val Met Leu Glu
210 215 220

Asp Asp Val Arg Cys Ser Lys Asn Phe Leu Thr Ala Ile Lys Lys Val
225 230 235 240

Ile Ala Ser Leu Glu Gly Thr Tyr Trp Val Thr Leu Glu Phe Ser Lys
245 250 255

Leu Gly Tyr Ile Gly Lys Leu Tyr His Ser His Asp Leu Pro Arg Leu
260 265 270

Ala His Phe Leu Leu Met Phe Tyr Gln Glu Met Pro Cys Asp Trp Leu
275 280 285

Leu Thr His Phe Arg Gly Leu Leu Ala Gln Lys Asn Val Ile Arg Phe
290 295 300

Lys Pro Ser Leu Phe Gln His Met Gly Tyr Tyr Ser Ser Tyr Lys Gly
305 310 315 320

Thr Glu Asn Lys Leu Lys Asp Asp Asp Phe Glu Glu Glu Ser Phe Asp
325 330 335

Ile Pro Asp Asn Pro Pro Ala Ser Leu Tyr Thr Asn Met Asn Val Phe
340 345 350

Glu Asn Tyr Glu Ala Ser Lys Ala Tyr Ser Ser Val Asp Glu Tyr Phe
355 360 365

Trp Gly Lys Pro Pro Ser Thr Gly Asp Val Phe Val Ile Val Phe Glu
370 375 380

Asn Pro Ile Ile Ile Lys Lys Ile Lys Val Asn Thr Gly Thr Glu Asp
385 390 395 400

Arg Gln Asn Asp Ile Leu His His Gly Ala Leu Asp Val Gly Glu Asn
405 410 415

Val Met Pro Ser Lys Gln Arg Gly Gln Cys Ser Thr Tyr Leu Arg Leu
420 425 430

Gly Glu Phe Lys Asn Gly Asn Phe Glu Met Ser Gly Val Asn Gln Lys
435 440 445

Ile Pro Phe Asp Ile His Cys Met Arg Ile Tyr Val Thr Lys Thr Gln
450 455 460

Lys Glu Trp Leu Ile Ile Arg Ser Ile Ser Ile Trp Thr Ser
465 470 475

<210> 9

<211> 1005

<212> DNA

<213> Homo sapiens

<400> 9

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ctcatggcgc tgctgccat cttttcgcc gcccgtggct ccgtacgctg cgcccgccgc	180
aagaatgctt cagacatgcc taaaaacaatc accagccggg atgcccggccg cttccccatc	240
atcgccagct gcacactctt gggctctac ctcttttca aaatattctc ccaggagttac	300
atcaacctcc tgctgtccat gtattttttc gtgctggaa tcctggccct gtcccacacc	360
atcagccccct tcatgaataa gttttttcca gccagcttcc caaatcgaca gtaccagctg	420

ctcttcacac agggttctgg ggaaaacaag gaagagatca tcaatttatga atttgacacc 480
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gtatggca ccaatgtgat ggtgacagtg gccaaagtcc tcgaggcacc aataaaattg 600
gtgttcccc aggatctgct ggagaaaggc ctcgaagcaa acaactttgc catgctggga 660
cttggagatg tcgtcattcc agggatcttc attgccttgc tgctgcgcct tgacatcagc 720
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atgttcagtt atgaggagtc aaatcctaag gatccagcgg cagtgacaga atccaaagag 960
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<210> 10
<211> 1486
<212> DNA
<213> Homo sapiens

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<223> Clone OA004b derived from T98G cell

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Met
1

gac tcg gcc ctc agc gat ccg cat aac ggc agt gcc gag gca ggc ggc 167
Asp Ser Ala Leu Ser Asp Pro His Asn Gly Ser Ala Glu Ala Gly Gly
5 10 15

ccc acc aac agc act acg cggtt ccgtt tcc acgtt ccc gag ggc atc gct 215
Pro Thr Asn Ser Thr Arg Pro Pro Ser Thr Pro Glu Gly Ile Ala
20 25 30

ctg gcc tac ggc agc ctc ctg ctc atg gctt ctg ccc atc ttc ttc 263
Leu Ala Tyr Gly Ser Leu Leu Met Ala Leu Leu Pro Ile Phe Phe
35 40 45

ggc gcc ctg cgc tcc gta cgc tgc gcc cgc ggc aag aat gct tca gac		311
Gly Ala Leu Arg Ser Val Arg Cys Ala Arg Gly Lys Asn Ala Ser Asp		
50	55	60
55	60	65
atg cct gaa aca atc acc agc cgg gat gcc gcc cgc ttc ccc atc atc		359
Met Pro Glu Thr Ile Thr Ser Arg Asp Ala Ala Arg Phe Pro Ile Ile		
70	75	80
75	80	
gcc agc tgc aca ctc ttg ggg ctc tac ctc ttt ttc aaa ata ttc tcc		407
Ala Ser Cys Thr Leu Leu Gly Leu Tyr Leu Phe Phe Lys Ile Phe Ser		
85	90	95
90	95	
cag gag tac atc aac ctc ctg ctg tcc atg tat ttc ttc gtg ctg gga		455
Gln Glu Tyr Ile Asn Leu Leu Ser Met Tyr Phe Phe Val Leu Gly		
100	105	110
105	110	
atc ctg gcc ctg tcc cac acc atc agc ccc ttc atg aat aag ttt ttt		503
Ile Leu Ala Leu Ser His Thr Ile Ser Pro Phe Met Asn Lys Phe Phe		
115	120	125
120	125	
cca gcc agc ttt cca aat cga cag tac cag ctg ctc ttc aca cag ggt		551
Pro Ala Ser Phe Pro Asn Arg Gln Tyr Gln Leu Leu Phe Thr Gln Gly		
130	135	140
135	140	145
tct ggg gaa aac aag gaa gag atc atc aat tat gaa ttt gac acc aag		599
Ser Gly Glu Asn Lys Glu Glu Ile Ile Asn Tyr Glu Phe Asp Thr Lys		
150	155	160
155	160	
gac ctg gtg tgc ctg ggc ctg agc agc atc gtt ggc gtc tgg tac ctg		647
Asp Leu Val Cys Leu Gly Leu Ser Ser Ile Val Gly Val Trp Tyr Leu		
165	170	175
170	175	
ctg agg aag gta ttt ggc acc aat gtg atg gtg aca gtg gcc aag tcc		695
Leu Arg Lys Val Phe Gly Thr Asn Val Met Val Thr Val Ala Lys Ser		
180	185	190
185	190	
ttc gag gca cca ata aaa ttg gtg ttt ccc cag gat ctg ctg gag aaa		743
Phe Glu Ala Pro Ile Lys Leu Val Phe Pro Gln Asp Leu Leu Glu Lys		
195	200	205
195	200	205
ggc ctc gaa gca aac aac ttt gcc atg ctg gga ctt gga gat gtc gtc		791
Gly Leu Glu Ala Asn Asn Phe Ala Met Leu Gly Leu Gly Asp Val Val		
210	215	220
215	220	225
att cca ggg atc ttc att gcc ttg ctg ctg cgc ttt gac atc agc ttg		839
Ile Pro Gly Ile Phe Ala Leu Leu Leu Arg Phe Asp Ile Ser Leu		
230	235	240
230	235	240
aag aag aat acc cac acc tac acc tac acc agc ttt gca gcc tac atc		887
Lys Lys Asn Thr His Thr Tyr Phe Tyr Thr Ser Phe Ala Ala Tyr Ile		
245	250	255
245	250	255
ttc ggc ctg ggc ctt acc atc ttc atc atg cac atc ttc aag cat gct		935
Phe Gly Leu Gly Leu Thr Ile Phe Ile Met His Ile Phe Lys His Ala		
260	265	270
265	270	

cag cct gcc ctc cta tac ctg gtc ccc gcc tgc atc ggt ttt cct gtc		983	
Gln Pro Ala Leu Leu Tyr Leu Val Pro Ala Cys Ile Gly Phe Pro Val			
275	280	285	
ctg gtg gcg ctg gcc aag gga gaa gtg aca gag atg ttc agt tat gag		1031	
Leu Val Ala Leu Ala Lys Gly Glu Val Thr Glu Met Phe Ser Tyr Glu			
290	295	300	305
gag tca aat cct aag gat cca gcg gca gtg aca gaa tcc aaa gag gga		1079	
Glu Ser Asn Pro Lys Asp Pro Ala Ala Val Thr Glu Ser Lys Glu Gly			
310	315	320	
aca gag gca tca gca tcg aag ggg ctg gag aag aaa gag aaa		1121	
Thr Glu Ala Ser Ala Ser Lys Gly Leu Glu Lys Lys Glu Lys			
325	330	335	
tgatgcggct ggtgcccgag cctctcaggg ccagaccaga cagatggggg ctggcccac		1181	
acaggcgtgc accggtagag ggcacaggag gccaaggga gctccaggac agggcagggg		1241	
gcagcaggat acctccagcc aggccctctgt ggccctctgtt tccttctccc tttttggcc		1301	
ctcctctgct cctccccaca ccctgcaggg aaaagaaaacc cccagcttcc cccctccccg		1361	
ggagccaggt gggaaaagtg ggtgtgattt ttagattttg tattgtggac tgattttgcc		1421	
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<211> 335
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Clone OA004b derived from T98G cell

<400> 11

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Gly Pro Thr Asn Ser Thr Thr Arg Pro Pro Ser Thr Pro Glu Gly Ile		
20	25	30

Ala Leu Ala Tyr Gly Ser Leu Leu Leu Met Ala Leu Leu Pro Ile Phe		
35	40	45

Phe Gly Ala Leu Arg Ser Val Arg Cys Ala Arg Gly Lys Asn Ala Ser
50 55 60

Asp Met Pro Glu Thr Ile Thr Ser Arg Asp Ala Ala Arg Phe Pro Ile
65 70 75 80

Ile Ala Ser Cys Thr Leu Leu Gly Leu Tyr Leu Phe Phe Lys Ile Phe
85 90 95

Ser Gln Glu Tyr Ile Asn Leu Leu Leu Ser Met Tyr Phe Phe Val Leu
100 105 110

Gly Ile Leu Ala Leu Ser His Thr Ile Ser Pro Phe Met Asn Lys Phe
115 120 125

Phe Pro Ala Ser Phe Pro Asn Arg Gln Tyr Gln Leu Leu Phe Thr Gln
130 135 140

Gly Ser Gly Glu Asn Lys Glu Glu Ile Ile Asn Tyr Glu Phe Asp Thr
145 150 155 160

Lys Asp Leu Val Cys Leu Gly Leu Ser Ser Ile Val Gly Val Trp Tyr
165 170 175

Leu Leu Arg Lys Val Phe Gly Thr Asn Val Met Val Thr Val Ala Lys
180 185 190

Ser Phe Glu Ala Pro Ile Lys Leu Val Phe Pro Gln Asp Leu Leu Glu
195 200 205

Lys Gly Leu Glu Ala Asn Asn Phe Ala Met Leu Gly Leu Gly Asp Val
210 215 220

Val Ile Pro Gly Ile Phe Ile Ala Leu Leu Leu Arg Phe Asp Ile Ser
225 230 235 240

Leu Lys Lys Asn Thr His Thr Tyr Phe Tyr Thr Ser Phe Ala Ala Tyr
245 250 255

Ile Phe Gly Leu Gly Leu Thr Ile Phe Ile Met His Ile Phe Lys His
260 265 270

Ala Gln Pro Ala Leu Leu Tyr Leu Val Pro Ala Cys Ile Gly Phe Pro
275 280 285

Val Leu Val Ala Leu Ala Lys Gly Glu Val Thr Glu Met Phe Ser Tyr
290 295 300

Glu Glu Ser Asn Pro Lys Asp Pro Ala Ala Val Thr Glu Ser Lys Glu
305 310 315 320

Gly Thr Glu Ala Ser Ala Ser Lys Gly Leu Glu Lys Lys Glu Lys
325 330 335

<210> 12
<211> 1080
<212> DNA
<213> Homo sapiens

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agtcaactag tgaattcaaa caacttgaag ctcaatttct ggaaatctcc ctccctccttc 180
aatcggcctg tggatgtcct ggtcccatct gtcagtcgc aggcatttaa atccttcctg 240
agatcccagg gcttagagta cgcatgtaca attgaggacc tgcaggccct tttagacaat 300
gaagatgatg aaatgcaaca caatgaaggg caagaacgga gcagtaataa cttcaactac 360
ggggcttacc attccctgga agctatttac cacgagatgg acaacattgc cgcagacttt 420
cctgacctgg cgaggagggt gaagattgga cattcgtttgc aaaaccggcc gatgtatgta 480
ctgaagttca gcactggaa aggcttgagg cggccggccg tttggctgaa tgcaggcatc 540
cattccccag agtggatctc ccaggccact gcaatctgga cggcaaggaa gattgtatct 600
gattaccaga gggatccagc tatcacctcc atcttggaga aaatggatat tttcttggtg 660
cctgtggcca atcctgatgg atatgtgtat actcaaactc aaaaccgatt atggaggaag 720
acgcggtccc gaaatcctgg aagctcctgc attggtgctg acccaaatacg aagctggAAC 780
gctagtttg cagggaaaggg agccagcgac aacccttgct ccgaagtgtt ccatggaccc 840
cacgccaatt cggaagtggaa ggtgaaatca gtggtagatt tcattccaaaa acatggaaat 900
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tcagtcaaaa aggccccaga tgccgaggaa ctcgacaagg tggcgaggct tgccggccaaa 1020
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<210> 13
 <211> 3156
 <212> DNA
 <213> Homo sapiens

<220>
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 <223> Clone OAF075b derived from human bone marrow stroma cell HAS303

<220>
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 Met Arg Trp Ile Leu Phe Ile Gly Ala Leu Ile Gly Ser
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agc atc tgt ggc caa gaa aaa ttt ttt ggg gac caa gtt ttt agg att 97
 Ser Ile Cys Gly Gln Glu Lys Phe Phe Gly Asp Gln Val Phe Arg Ile
 -1 1 5 10

aat gtc aga aat gga gac gag atc agc aaa ttg agt caa cta gtg aat 145
 Asn Val Arg Asn Gly Asp Glu Ile Ser Lys Leu Ser Gln Leu Val Asn
 15 20 25

tca aac aac ttg aag ctc aat ttc tgg aaa tct ccc tcc tcc ttc aat 193
 Ser Asn Asn Leu Lys Leu Asn Phe Trp Lys Ser Pro Ser Ser Phe Asn
 30 35 40 45

cgg cct gtg gat gtc ctg gtc cca tct gtc agt ctg cag gca ttt aaa 241
 Arg Pro Val Asp Val Leu Val Pro Ser Val Ser Leu Gln Ala Phe Lys
 50 55 60

tcc ttc ctg aga tcc cag ggc tta gag tac gca gtg aca att gag gac 289
 Ser Phe Leu Arg Ser Gln Gly Leu Glu Tyr Ala Val Thr Ile Glu Asp
 65 70 75

ctg cag gcc ctt tta gac aat gaa gat gat gaa atg caa cac aat gaa 337
 Leu Gln Ala Leu Leu Asp Asn Glu Asp Asp Glu Met Gln His Asn Glu
 80 85 90

ggg caa gaa cgg agc agt aat aac ttc aac tac ggg gct tac cat tcc Gly Gln Glu Arg Ser Ser Asn Asn Phe Asn Tyr Gly Ala Tyr His Ser	385
95 100 105	
ctg gaa gct att tac cac gag atg gac aac att gcc gca gac ttt cct Leu Glu Ala Ile Tyr His Glu Met Asp Asn Ile Ala Ala Asp Phe Pro	433
110 115 120 125	
gac ctg gcg agg agg gtg aag att gga cat tcg ttt gaa aac cgg ccg Asp Leu Ala Arg Arg Val Lys Ile Gly His Ser Phe Glu Asn Arg Pro	481
130 135 140	
atg tat gta ctg aag ttc agc act ggg aaa ggc gtg agg cgg ccg gcc Met Tyr Val Leu Lys Phe Ser Thr Gly Lys Gly Val Arg Arg Pro Ala	529
145 150 155	
gtt tgg ctg aat gca ggc atc cat tcc cga gag tgg atc tcc cag gcc Val Trp Leu Asn Ala Gly Ile His Ser Arg Glu Trp Ile Ser Gln Ala	577
160 165 170	
act gca atc tgg acg gca agg aag att gta tct gat tac cag agg gat Thr Ala Ile Trp Thr Ala Arg Lys Ile Val Ser Asp Tyr Gln Arg Asp	625
175 180 185	
cca gct atc acc tcc atc ttg gag aaa atg gat att ttc ttg ttg cct Pro Ala Ile Thr Ser Ile Leu Glu Lys Met Asp Ile Phe Leu Leu Pro	673
190 195 200 205	
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210 215 220	
tgg agg aag acg cgg tcc cga aat cct gga agc tcc tgc att ggt gct Trp Arg Lys Thr Arg Ser Arg Asn Pro Gly Ser Ser Cys Ile Gly Ala	769
225 230 235	
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240 245 250	
gac aac cct tgc tcc gaa gtg tac cat gga ccc cac gcc aat tcg gaa Asp Asn Pro Cys Ser Glu Val Tyr His Gly Pro His Ala Asn Ser Glu	865
255 260 265	
gtg gag gtg aaa tca gtg gta gat ttc atc caa aaa cat ggg aat ttc Val Glu Val Lys Ser Val Val Asp Phe Ile Gln Lys His Gly Asn Phe	913
270 275 280 285	
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290 295 300	
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305

310

315

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Val Ala Arg Leu Ala Ala Lys Ala Leu Ala Ser Val Ser Gly Thr Glu																																																							
320	325	330		tac caa gtg ggt ccc acc tgc acc act gtc tta taaactgccaa aaactggag	1110	Tyr Gln Val Gly Pro Thr Cys Thr Thr Val Leu		335	340	atactcatca gattgctcca acagaagagg aggaaggctc tcccggggc tgtccaggag	1170	acataaaaatt tctacctttt cttttctttt tgaaatggag ttgcgtttcg ctcttgtgc	1230	ccaggctgga gtgcaatggc gtgatctcca ctcatcgcaa cttccgcctc ccaggttcaa	1290	gcgattcccc tgcctcagcc tcccgagtaa ctgggattat aggcatgtgc cccaccccca	1350	actaattttt gtatttttag tagagatggg gtttctccat gttggtcagt ctggcttga	1410	gctcccgacc tcaggtgatc tgccgcctc ggcctctcaa agtgctggga ttacaggcgt	1470	gagccacagc acccggccaa aatgtccacc ttttctaaga gcccattttc catattctt	1530	ataggccttgc tctgtccttg tttttcaaa aaaaaaaacaa tcaatttttgc tataatagca	1590	ctctatccaa cgccataggt tatggtgtgt gctacataca cagtcgacgt ttgtccttgc	1650	aagtgcgtgg cctttctca gatgccatt ttagaggaaa ataattctaa aatggatttt	1710	acactcttct gccttctaaa acagagcatg gagaagagat ttaagccctt ttttcatgg	1770	ttaagtgtac ttctcaacct cagttcgat atgctaaagg cctactctgc cgtcttggac	1830	tgtttggacc ttctgctaaa tgatcctggc ctgtttcct tcttgcgttt gctttgtaga	1890	tttttgtgtc tcctttctcc tgccagactg tcagcagtag cttgtattgc ttcaggccaa	1950	cagcctctag caacccttcc ccctcctctt cactgattct gctccaggaa gggcttggaa	2010	acaagttctt tgggttcatc tgacttgcgtt ataacacagt ttcatgtact ttttgcgtt	2070	cataagcgtg gtgattgggt tttcacgctc atgtgtgaca tatgccttcc tccaatttttgc	2130	ttacaatgtt ggtgcgttac ccatcagaca tggggaaaga aagggtgttc atgacagcat	2190	tatccatagt tacaaaagac atgtacaggg gccaaggaa aacttccct ttgccttctg	2250	aaggttcatt gaaaaatcaa ctgaccaaaag gcagatcgat aggagaaaag gcataaaaaa	2310	ttttatgttta gtgtgcgttac cacagggaa tcacaggaga atgatttccc aataacccaa	2370	tggggcacag aagcttgcgtt acccttttc atacaggagg gaggagatgt atggactggg	2430	gaggtggag gcagatatta caggaaggtg agggggcggag ctgtacagga acaaagcttgc	2490
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Tyr Gln Val Gly Pro Thr Cys Thr Thr Val Leu																																																							
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Asn Gly Asp Glu Ile Ser Lys Leu Ser Gln Leu Val Asn Ser Asn Asn
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Leu Lys Leu Asn Phe Trp Lys Ser Pro Ser Ser Phe Asn Arg Pro Val
35 40 45

Asp Val Leu Val Pro Ser Val Ser Leu Gln Ala Phe Lys Ser Phe Leu
50 55 60

Arg Ser Gln Gly Leu Glu Tyr Ala Val Thr Ile Glu Asp Leu Gln Ala
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Leu Leu Asp Asn Glu Asp Asp Glu Met Gln His Asn Glu Gly Gln Glu
85 90 95

Arg Ser Ser Asn Asn Phe Asn Tyr Gly Ala Tyr His Ser Leu Glu Ala
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Ile Tyr His Glu Met Asp Asn Ile Ala Ala Asp Phe Pro Asp Leu Ala
115 120 125

Arg Arg Val Lys Ile Gly His Ser Phe Glu Asn Arg Pro Met Tyr Val
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Leu Lys Phe Ser Thr Gly Lys Gly Val Arg Arg Pro Ala Val Trp Leu
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Asn Ala Gly Ile His Ser Arg Glu Trp Ile Ser Gln Ala Thr Ala Ile
165 170 175

Trp Thr Ala Arg Lys Ile Val Ser Asp Tyr Gln Arg Asp Pro Ala Ile
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Thr Ser Ile Leu Glu Lys Met Asp Ile Phe Leu Leu Pro Val Ala Asn
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Pro Asp Gly Tyr Val Tyr Thr Gln Thr Gln Asn Arg Leu Trp Arg Lys
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Thr Arg Ser Arg Asn Pro Gly Ser Ser Cys Ile Gly Ala Asp Pro Asn
225 230 235 240

Arg Ser Trp Asn Ala Ser Phe Ala Gly Lys Gly Ala Ser Asp Asn Pro
245 250 255

Cys Ser Glu Val Tyr His Gly Pro His Ala Asn Ser Glu Val Glu Val
260 265 270

Lys Ser Val Val Asp Phe Ile Gln Lys His Gly Asn Phe Lys Cys Phe

275

280

285

Ile Asp Leu His Ser Tyr Ser Gln Leu Leu Met Tyr Pro Tyr Gly Tyr
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Ser Val Lys Lys Ala Pro Asp Ala Glu Glu Leu Asp Lys Val Ala Arg
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